(FILE 'HOME' ENTERED AT 10:50:50 ON 21 FEB 2003)

FILE 'MEDLINE, CANCERLIT, BIOTECHDS, EMBASE, BIOSIS, CAPLUS' ENTERED AT 10:51:03 ON 21 FEB 2003

L1	767750	S	POLYMERASE
L2	106413	S	ADENOVIR?
L3	1333	S	ITR
L4	414820	S	HAIRPIN OR COMPLEMENTARY
L5	59561	S	L4 AND L1
L6	472	S	L5 AND L2
L7	288		DUP REM L6 (184 DUPLICATES REMOVED)
L8	8	S	L7 AND LINEAR
L9	91889	S	NUCLEIC ACID POLYMERASE OR DNA POLYMERASE
L10	50	S	L9 AND L6
L11	30		DUP REM L10 (20 DUPLICATES REMOVED)
L12	86782	S	SINGLE STRANDED
L13	182	S	L12 AND L4 AND L2
L14	0	S	L13 AND HAIPRIN
L15	80		DUP REM L13 (102 DUPLICATES REMOVED)
L16	0	S	L15 AND COMPLEMNENTARY
L17	80	S	L15 AND L4
L18	3	S	L17 AND L9

L17 ANSWER 10 OF 80 MEDLINE
AN 94300598 MEDLINE
DN 94300598 PubMed ID: 8028005
TI Structural study of the 5' end of a synthetic premessenger RNA from **adenovirus**. Evidence for a long-range exon-intron interaction.
AU Gallinaro H; Domenjoud L; Jacob M
CS Laboratoire de Genetique Moleculaire des Eucaryotes du CNRS, Faculte de Medecine, Strasbourg, France.
SO JOURNAL OF MOLECULAR BIOLOGY, (1994 Jul 15) 240 (3) 205-25.
Journal code: 2985088R. ISSN: 0022-2836.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-S71400
EM 199408
ED Entered STN: 19940818
Last Updated on STN: 19970203
Entered Medline: 19940809
AB In order to establish the structural features of the cis-elements involved in splicing and in its regulation, we have analyzed a synthetic premessenger RNA, derived from the E3 transcription unit of **adenovirus**-2 and previously shown to be a good substrate for in vitro splicing. The transcript was probed by enzymatic and chemical methods and we present the structure in solution of the upstream exon and of the 5' part of the intron. This 417 nucleotide long fragment, which overlaps the exon-intron junction harbors the natural 5' splice site D1 and an intronic cryptic site, Dcr1, used when D1 is suppressed. The 5' exon is folded in three stem-loop structures and D1 is located in a free **single-stranded** region close to the foot of the most stable of these structures (ex1-HP1). The 5' part of the intron also contains a stable **hairpin** structure (IVS1-hp1), which sequesters Dcr1. The different structural context of the two 5' splice sites may partly explain the selection of D1 and the silencing of Dcr1. We also found a long-range, 20 base-pair, exon-intron interaction, which agrees with the enzymatic and chemical probings and was further demonstrated by the study of the colinear messenger RNA, lacking the intron and of 5' deletion transcripts, lacking the 5' part of the exon. This folding creates a three-branched structure, including IVS1-hp1 and divides the 5' part of the transcript into two domains. Finally, only a few sequences are not involved in folded structures. Free **single-stranded** fragments are found between the exonic hairpins and at the beginning of the intron and are mostly U-rich. All the structural features of the **adenovirus**-2 transcript are conserved in **adenovirus**-5, in spite of 37 nucleotide substitutions.

L17 ANSWER 20 OF 80 MEDLINE
AN 89088256 MEDLINE
DN 89088256 PubMed ID: 3264727
TI **Adenovirus** DNA replication in vitro: duplication of **single-stranded** DNA containing a panhandle structure.
AU Leegwater P A; Rombouts R F; van der Vliet P C
CS Laboratory for Physiological Chemistry, State University of Utrecht, The Netherlands.
SO BIOCHIMICA ET BIOPHYSICA ACTA, (1988 Dec 20) 951 (2-3) 403-10.
Journal code: 0217513. ISSN: 0006-3002.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 198902
ED Entered STN: 19900308
Last Updated on STN: 19900308
Entered Medline: 19890213
AB **Adenovirus** DNA replicates by displacement of one of the parental strands followed by duplication of the displaced parental single strand (**complementary** strand synthesis). Displacement synthesis has been performed in a reconstituted system composed of viral and cellular proteins, employing either the viral DNA-terminal protein complex as template or linearized plasmids containing the origin. Previously, evidence was obtained that in vivo **complementary** strand synthesis requires formation of a panhandle structure originating from hybridization of the inverted terminal repeats. To study the conditions for **complementary** strand synthesis in vitro, we have constructed an artificial panhandle molecule that contains a double-stranded inverted terminal repetition (ITR) region and a **single-stranded** loop derived from the left and right terminal XmaI fragments of Ad2. Such a molecule appeared to be an efficient template and could initiate by the same protein-priming mechanism as double-stranded DNA, employing the precursor terminal protein. The efficiency of both types of template was comparable. Like for replication of the duplex molecule initiation of panhandle replication was stimulated by nuclear factors I and III, proteins that bind to specific double-stranded regions of the ITR. The Ad DNA-binding protein is essential and the 39 kDa C-terminal domain of this protein that harbors the DNA-binding properties is sufficient for its function. These results support the hypothesis that panhandle formation is required for duplication of the displaced strand.

L17 ANSWER 28 OF 80 MEDLINE
AN 77097304 MEDLINE
DN 77097304 PubMed ID: 833948
TI Structure of the inverted terminal repetition of **adenovirus** type 2 DNA.
AU Wu M; Roberts R J; Davidson N
SO JOURNAL OF VIROLOGY, (1977 Feb) 21 (2) 766-77.
Journal code: 0113724. ISSN: 0022-538X.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 197703
ED Entered STN: 19900313
Last Updated on STN: 19900313
Entered Medline: 19770331
AB Several secondary structure features involving the ends of single strands of **adenovirus** type 2 DNA have been studied by electron microscopy by both the gene 32-ethidium bromide technique and a modification of the standard formamide-cytochrome c technique. A duplex stem of length 115 +/- 10 nucleotide pairs due to pairing between the two members of the inverted terminal repetition is observed in the **single-stranded** circles that form upon annealing **single-stranded** linear molecules. This duplex stem is shown to lie at the ends of the DNA by using several reference markers: (i) a newly discovered secondary structure feature (a loop of length ca. 500 nucleotides with a 20-nucleotide pair duplex stem) that maps 73% of the full length from the left end of the molecule and (ii) a duplex region due to a hybridized restriction fragment. There is also some secondary structure within each end of linear single strands. There is some variation in the morphology of the end strucures, and we propose that these involve base pairing, as in a tRNA clover leaf, rather than an exact single **hairpin**-type inverted repeat. These observations are consistent with the hypothesis that there is a foldback structure at the 3' ends of the DNA that functions as a primer for the initiation of replication.

L17 ANSWER 29 OF 80 MEDLINE
AN 76027907 MEDLINE
DN 76027907 PubMed ID: 1165594
TI Isolation and partial characterization of **single-stranded adenoviral** DNA produced during synthesis of **adenovirus** type 2 DNA.
AU Lavelle G; Patch C; Khoury G; Rose J
SO JOURNAL OF VIROLOGY, (1975 Oct) 16 (4) 775-82.
Journal code: 0113724. ISSN: 0022-538X.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Abridged Index Medicus Journals; Priority Journals
EM 197512
ED Entered STN: 19900313
Last Updated on STN: 19900313
Entered Medline: 19751211
AB **Single-stranded** fragments of **adenovirus** type 2 DNA were isolated from infected KB cells under conditions which retarded reassociation of **complementary** sequences but did not denature native viral DNA. Of the total intracellular, virus-specific DNA labeled during a 1-h pulse with tritiated thymidine begining 15 h after infection, about 20% was **single stranded** when fractionated on hydroxylapatite. This DNA shifted predominantly to the double-stranded fraction on hydroxylapatite during an extended chase incubation, suggesting that it may represent **single-stranded** DNA in replicating intermediates. Furthermore, the **single-stranded** DNA annealed nearly equally to both strands of the **adenovirus** genome. These findings indicate that at least portions of both **complementary** strands of **adenovirus** type 2 DNA are exposed as single strands during the period of viral DNA synthesis.

L17 ANSWER 30 OF 80 MEDLINE

L11 ANSWER 27 OF 30 CANCERLIT DUPLICATE 9
AN 76702992 CANCERLIT
DN 76702992
TI EVIDENCE FOR PALINDROMIC SEQUENCES NEAR THE TERMINI OF **ADENOVIRUS** 2 DNA.
AU Padmanabhan R; Padmanabhan R; Green M
CS St. Louis Univ. Sch. Medicine, 3861 Park Ave., St. Louis, MO 63110.
SO Biochem Biophys Res Commun, (1976) 69 (4) 860-867.
ISSN: 0006-291X.
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Cancer Assessment Review Committee
EM 197611
ED Entered STN: 19941107
Last Updated on STN: 19941107
AB The kinetics of Escherichia coli exonuclease III digestion of **adenovirus** 2 DNA were studied by **DNA polymerase** I-catalyzed repair synthesis at 5 C. The results suggested the formation of a **hairpin** structure in the single-stranded template, exposed by endonuclease III. This structure resulted from a sequence with an inverted repetition of the type a b c d;;;d' c' b' a'. These sequences were approximately 180 nucleotides from each terminus of **adenovirus** 2 DNA, as determined by the use of specific restriction endonucleases. The possible role of this region in the replication of the **adenovirus** 2 genome is discussed.

L11 ANSWER 27 OF 30 CANCERLIT DUPLICATE 9
AN 76702992 CANCERLIT
DN 76702992
TI EVIDENCE FOR PALINDROMIC SEQUENCES NEAR THE TERMINI OF **ADENOVIRUS** 2 DNA.
AU Padmanabhan R; Padmanabhan R; Green M
CS St. Louis Univ. Sch. Medicine, 3861 Park Ave., St. Louis, MO 63110.
SO Biochem Biophys Res Commun, (1976) 69 (4) 860-867.
ISSN: 0006-291X.
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Cancer Assessment Review Committee
EM 197611
ED Entered STN: 19941107
Last Updated on STN: 19941107
AB The kinetics of Escherichia coli exonuclease III digestion of **adenovirus** 2 DNA were studied by **DNA polymerase** I-catalyzed repair synthesis at 5 C. The results suggested the formation of a **hairpin** structure in the single-stranded template, exposed by endonuclease III. This structure resulted from a sequence with an inverted repetition of the type a b c d;;;d' c' b' a'. These sequences were approximately 180 nucleotides from each terminus of **adenovirus** 2 DNA, as determined by the use of specific restriction endonucleases. The possible role of this region in the replication of the **adenovirus** 2 genome is discussed.

L8 ANSWER 4 OF 8 CANCERLIT
AN 77703205 CANCERLIT
DN 77703205
TI THE STRUCTURE AND REPLICATION OF THE **ADENOVIRUS** GENOME.
AU Pearson G D
SO Non-serial, (1976) The Biology of Tumor Viruses Proceedings of the Thirty-fourth Annual Biology Colloquium. Beaudreau GS, Synder S, ed. Corvallis, Oregon State University Press, 1976. .
DT (GOVERNMENT REPORT)
LA English
FS Cancer Assessment Review Committee
EM 197705
ED Entered STN: 19941107
Last Updated on STN: 19941107
AB The DNA structure and replication of the closely related types 2 and 5 **adenoviruses** are reviewed. The **linear adenovirus** chromosome has a MW of 23 x 10**6. The sequence of the chromosome, determined by denaturation mapping, is not circularly permuted. Site-specific endonucleases cleave **adenovirus** DNA into unique fragments, permitting the topography of the chromosome to be defined completely. **Adenoviruses** replicate in the nuclei of infected cells. Viral DNA most likely exists within the nucleus as a nucleoprotein complex that contains two virus-specified DNA binding proteins as well as endonuclease and DNA **polymerase** activities. **Adenoviruses** replicate discontinuously, the average time required for replication being 26-27 min. Complete joining of daughter strands requires at least an additional 25-30 min. A replication map of **adenovirus** was constructed using the EcoRI restriction endonuclease. These data together with those from pulse-labeling experiments indicate that two replicative origins are positioned 25% from either end of the chromosome. The light alkaline strand is used as a template for leftward replication starting in fragment C and ending in fragment A. The heavy alkaline parental strand is displaced. There are four origins for rightward synthesis on the displaced strand: one at the left end, one 25% from the left end, one near the middle of the chromosome, and one in EcoRI-F. These distances roughly correspond to the sizes of unjoined daughter strands present in newly finished molecules. The **adenovirus** molecule is not terminally repetitious in the usual sense, but has an inverted terminal repetition. A model illustrating the structure and role of the inverted terminal repetition in **adenovirus** DNA indicates that the ends of the **linear** duplex molecule fold back as hairpins. As a consequence, the nucleotide sequence at the 3' terminus of one strand is not necessarily **complementary** to the sequence at the 5' terminus of the other strand. Another model for the replication of **linear** molecules that also involves **hairpin** ends has been proposed independently. Experiments are in progress to test for the presence of **hairpin** regions in the **adenovirus** chromosome. (48 refs)

L8 ANSWER 5 OF 8 CANCERLIT
AN 77703034 CANCERLIT
DN 77703034
TI THE MECHANISM OF REPLICATION OF **ADENOVIRUS** TYPE 5 DNA.
AU *Sussenbach J S; Van der Vliet P C; Ellens D J; Vlak J; Jansz H S*
SO Non-serial, (1975) Tumor Virus-Host Cell Interaction. Kolber A, ed. New York, Plenum Press, 1975. .
DT Book; (MONOGRAPH)
LA English
FS Cancer Assessment Review Committee
EM 197704
ED Entered STN: 19941107
Last Updated on STN: 19941107
AB The mechanism for the replication of **adenovirus** type 5 (Ad5) DNA was studied. To study viral DNA synthesis, isolated nuclei from Ad5-infected KB cells were incubated in a synthetic medium, and the DNA isolated thereafter was studied using sucrose gradient centrifugation. Three classes of new DNA were observed: one sedimenting faster than mature Ad5 DNA (I), one sedimenting slower (III), and one sedimenting with the same velocity (II). I and II contained replicative intermediates, but III contained cellular DNA plus fragments of replicative intermediates produced by shear. An extended study of the replicative intermediates indicated that they contained new DNA of genome length or shorter, that they contained single-stranded DNA, that the new DNA in them was not covalently linked to parental DNA, and that they had a **linear** structure. Based on these observations, a model was constructed for the replication of Ad5 DNA. In this model (the 1 model), DNA synthesis starts at the end of the **linear** duplex on one strand, displacing the other strand and producing one completed double-stranded daughter molecule and a single strand. The latter is converted into the other daughter molecule by discontinuous synthesis of a **complementary** strand. Alternatively, **complementary**-strand synthesis may start in the branched structure, ultimately leading to the same result. As predicted by the model, the new DNA formed by Ad5-infected cells was in double-stranded form, although a considerable fraction of the parental DNA in replicative intermediates was single-stranded. The replication of Ad5 DNA started always at the molecular right end of the **linear** duplex, displacing the viral heavy strand. This implies that the 5'-end of the viral H-strand is located at the molecular right end and that this end is recognized by an initiation factor or DNA **polymerase**. (11 refs)